

## FIG. 1

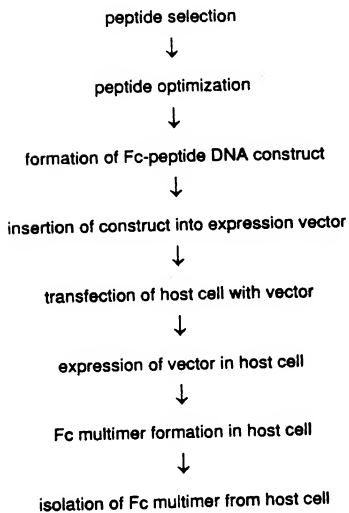


FIG. 2A

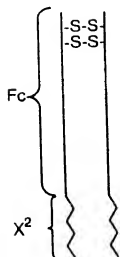


FIG. 2B

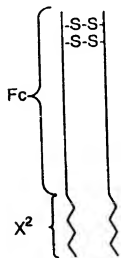


FIG. 2C

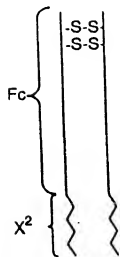


FIG. 2D

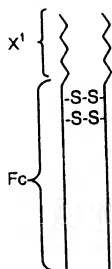


FIG. 2E

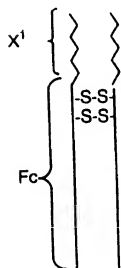


FIG. 2F

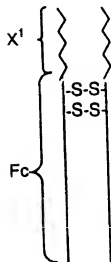


FIG. 3A

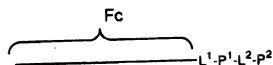


FIG. 3B

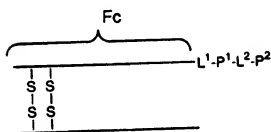
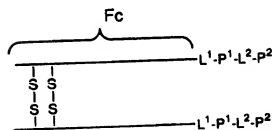


FIG. 3C



# FIG. 4

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ATGGACAAAACACACATGTCCACCTTGTCAGCTCCGGAACCTCTGGGGGGACCGTCA
1  TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCCTTGAGGACCCCCCTGGCAGT
a  M D K T H T C P P C P A P E L L G G P S
GTCTTCCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCGGACCCCTCGAGTGC
61  CAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCTCGGGACTCCAG
a  V F L F P P K P K D T L M I S R T P E V
ACATGCGTGGTGGTGGACGTGAGCCAGAACCCCTGAGGTCAAGTTCAACTGGTACGTCG
121  TGTACGCACCACCACCTGCACCTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC
a  T C V V V D V S H E D P E V K F N W Y V
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAACAGCAG
181  CTGCCGCACCTCCAGCTATTACGGTTCTGTTTCGGCGCCCTCTCTGCATGTTGTGCTGTC
a  D G V E V H N A K T K P R E E Q Y N S T
TACCGTGTGGTCAGCGTCTCTACCGTCTCTGCACAGACTGGCTGAATGCCAAGGAGTAC
241  ATGGACACACAGTCGAGGAGTGGCAGGACGTGGTCTCGACCGACTTACCGTTCTCATG
a  Y R V V S V L T V L H Q D W L N G K E Y
AAGTGCAAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
301  TTCACGTTCCAGAGGTTGTTTCGGGAGGTCGGGGGTAGCTCTTTGGTAGAGGTTTCGG
a  K C K V S N K A L P A P I E K T I S K A
AAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCCCATCCGGGATGAGCTGACC
361  TTTCCTGTCGGGGCTCTTGGTGTCACATGTGGGACGGGGTAGGGCCCTACTCGACTGG
a  K G Q P R E P Q V Y T L P P S R D E L T
AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTG
421  TTCTTGGTGCAGTCGAGCTGGACGGACCAAGTTTCGGAAGATAGGGTCGCTGATAGCGGCAC
a  K N Q V S L T C L V K G F Y P S D I A V
GAGTGGGAGAGCAATGGGACGCCGAGAACCACTACAAGACACCGCCTCCCGTGTGGAC
481  CTCACCCCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCACGACCTG
a  E W E S N G Q P E N N Y K T T P P V L D
TCCGACGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACCAAGAGCAGGTGGCAGCAG
541  AGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCTGTCACCGTCGTC
a  S D G S F F L Y S K L T V D K S R W Q Q
GGGAACGCTTCTCATGCTCCGTGATGCGATGAGGCTCTGCACAAACCTACACGAGAGG
601  CCGTTGCAGAAAGATACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC
a  G N V F S C S V M H E A L H N H Y T Q K
AGCCTCTCCCTGTCTCCGGGTAAA
661  TCGGAGAGGGACAGAGGCCCATTT

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FIG. 5

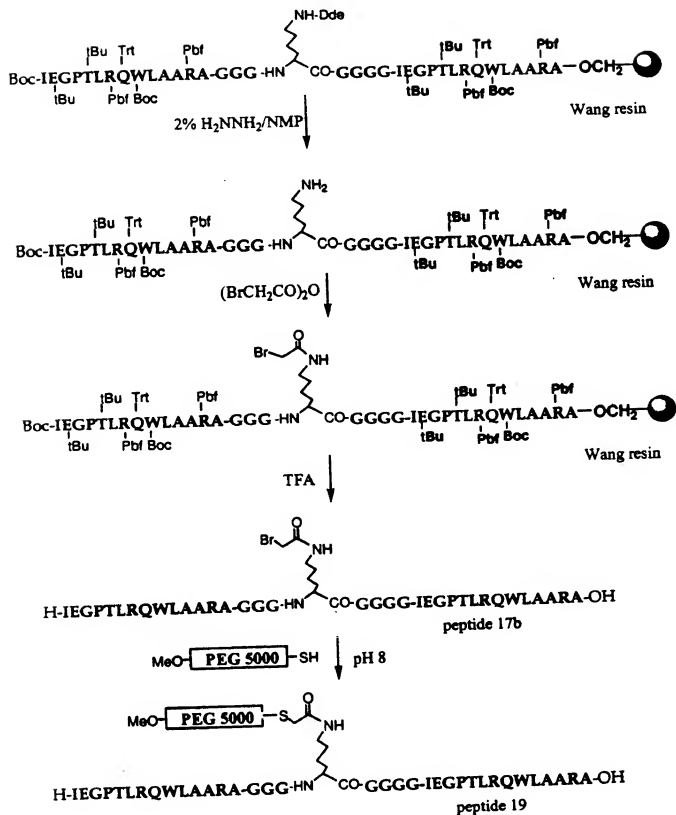


FIG. 6

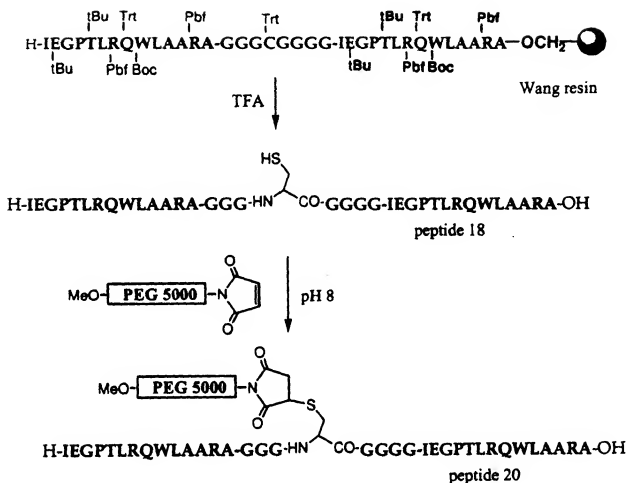
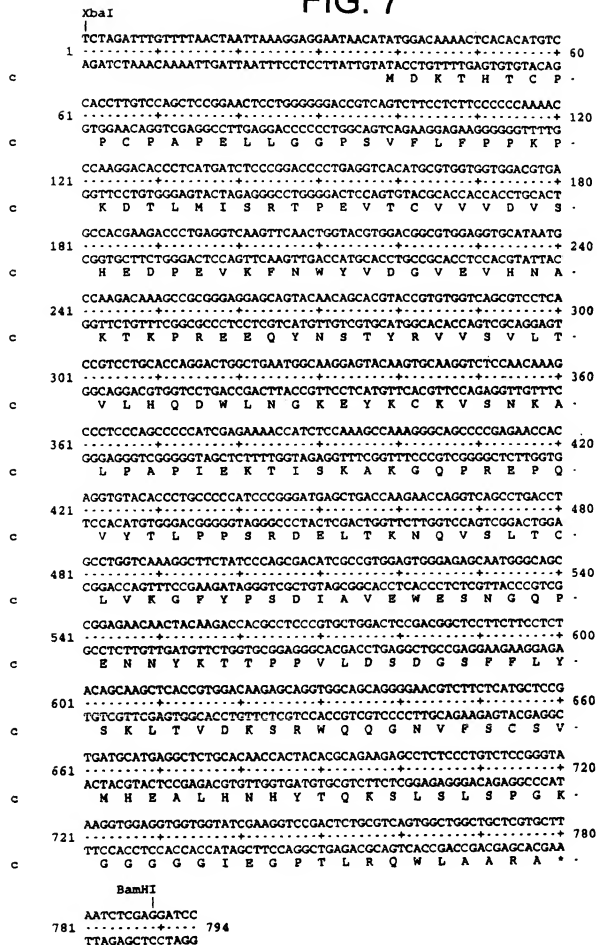


FIG. 7



# FIG. 8

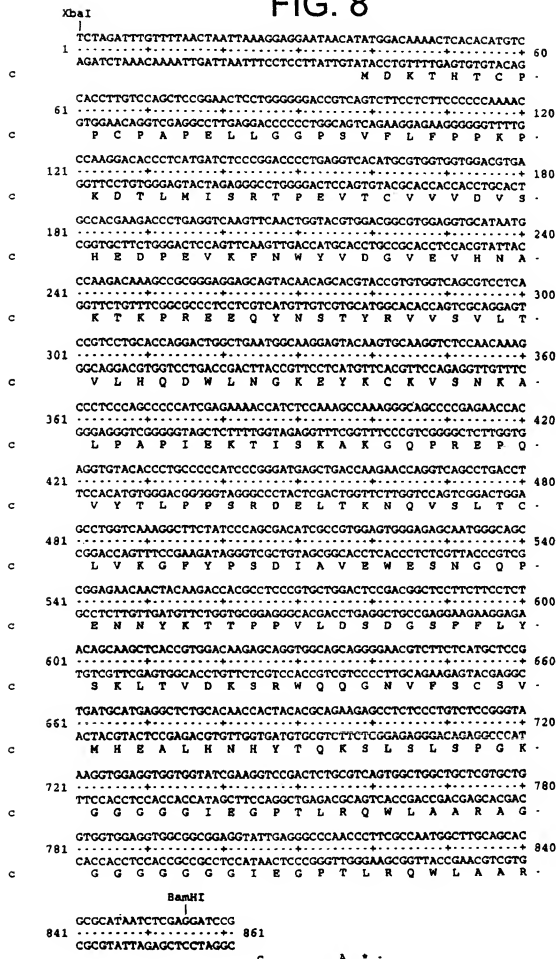
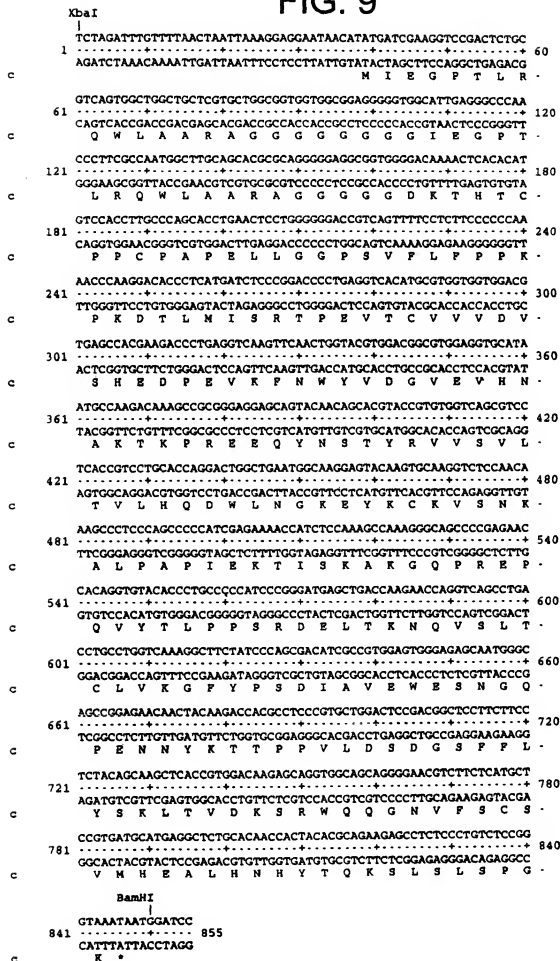




FIG. 9



# FIG. 10

	XbaI	
1	TCTAGATTGTTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCGCACTCTGC	
	AGATCTAAACAAAATGATTAAATTCCTCCTTATTGTATACAGTCTCCAGGCTGACAGC	60
c	M I E G P T L R	
	GTCACTGGCTGGCTGCTGCTGCTGGTGGAGGCGTGGGGACAAAACACACATGTCCAC	
61	CAGTCAACGACGACGAGCAGCAGCACCTCCGACACCCCTGTTTGTAGTGTGTACAGGTG	120
c	Q W L A A R A G G G G G D K T H T C P P	
	CTTGGCCAGCACCTGAACTCTGGGGGGACCGTCAGTTTTCCTTCCCCCAAAACCCA	
121	GAACGGTCTGTGGACTTGAGGACCCCTCGGACGTCAAAGGAGAAAGGGGGTTCCTGGGT	180
c	C P A P E L L G G P S V F L F P P K P K	
	AGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATCGCTGGTGGAGCGTGAGCC	
181	TCCTGTGGGAGTACTAGAGGGCTGGGAGTCCAGTGTACCCACCCACCTGCACCTCGG	240
c	D T L M I S R T F E V T C V V V D V S H	
	ACGAAGACCCCTGAGGTCAAGTTCACCTGGTACGTGGACGGCTGGAGGTGCATAATGCCA	
241	TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCGCCGACCTCCACGTATTACGGT	300
c	E D P E V K F N W Y V D G V E V H N A K	
	AGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCCACCG	
301	TCTGTTTCGGGCGCTCTCTGTCTATGTTGTCTGTGATGGACACACAGTCCGAGGAGTGGC	360
c	T K P R E E Q Y N S T Y R V V S V L T V	
	TCCTGCACCAAGACTGGCTGAATGGCAAGGAGTACAAGTCCAAGTCTCCAACAAGGCC	
361	AGGACGTGGTCTGACCGACTTACCGTTCCCTCATGTTACGTTCCAGAGGTGTTTCGGG	420
c	L H Q Q D W L N G K E Y K C K V S N K A L	
	TCCAGCCCCCATCGAGAAAACATCTCAAAGCCAAAGGCGAGCCCGAGAACACACAGG	
421	AGGTCGCGGGGTAGCTCTTTGGTAGAGGTTTCGGTTTCCTCGGGGCTCTTGGTGTCC	480
c	P A P I E K T I S K A K G Q P R E P Q V	
	TGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCGAGTCAAGCTGACCTGCC	
481	ACATGTGGGACGGGGGTAGGGCCCTACTGACTGTTCTTGGTCCAGTCCGAGTGGACGG	540
c	Y T L P P S R D E L T K N Q V S L T C L	
	TGGTCAAAGGCTTCTATCCAGCGACATGCCGTGGAGTGGGAGAGCAATGGCAGCCGG	
541	ACCAGTTTCCGAAGATAGGGTCTGTAGCGGACCTCACCCTCTCGTTACCGGTGCGGC	600
c	V K G F Y P S D I A V E W E S N G Q P E	
	AGAACAACCTACAAGACCAACGCTCCCGTCTGGACTCCGACGGCTCCTTCTTCTCTACA	
601	TCTTGTGTATGTTCTGGTCCGAGGGACGACCTGAGGCTGCCAGGAGAAAGGAGATGT	660
c	N N Y K T T P P V L D S D G S F F L Y S	
	GCAAGCTCACCCTGGACAAGAGCAGGTGGCAGAGGGGAACGTCTTCTCATGCTCCGTA	
661	CGTTCAGTGGCAGCTGTTCTCTGTCACGTGCTGCCCTTTCAGAGAAGTACGAGGCACT	720
c	K L T V D K S R W Q Q G N V F S C S V M	
	TGCATGAGGCTCTGCACAACCACTACACGCAAGAAGGCTCTTCCCTGTCTCCGGGTAAAT	
721	ACGTACTCCGAGACGTGTTGGTGTATGTCGCTTCTTCGAGAGGAGACAGAGCCCATTTA	780
c	H E A L H N H Y T Q K S L S L S P G K	
	BamHI	
	AATGGATCC	
781	TTACCTAGG	789

FIG.11

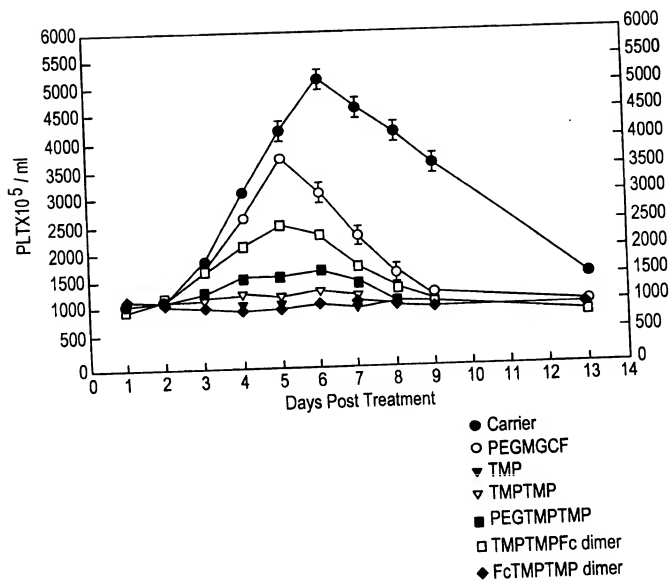
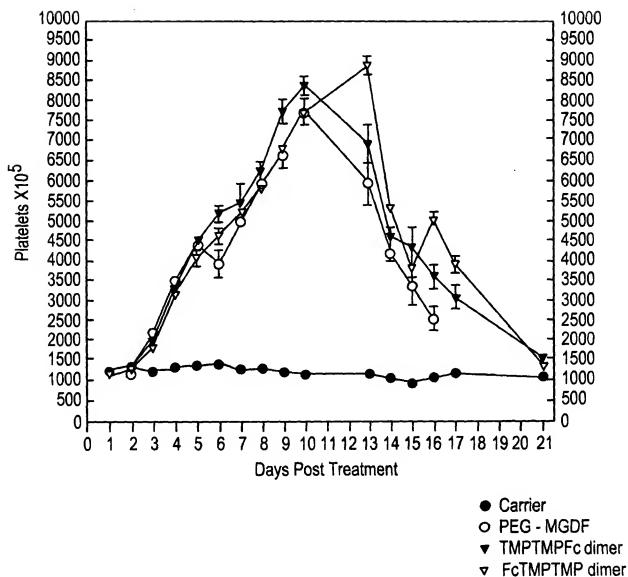


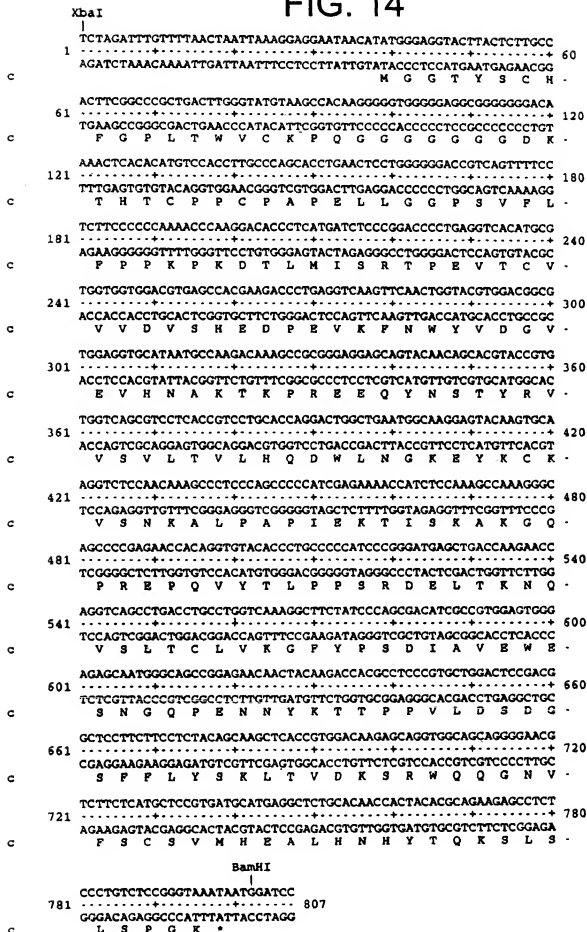
FIG.12



# FIG. 13

XbaI  
|  
TCTAGATTGTTTAACTAATTAAGGAGGAATAACATATGGACAAAACACACATGTC  
1 AGATCTAAACAAAATGATTAAATTTCTCCTTATTGTATACCTGTTTGTAGTGTGTACAG 60  
CACCTTGTCCAGCTCCGGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC  
61 GTGGAACAGGTGAGGCCTTGAGGACCCCTGGCAGTCAGAAGGAGAGGGGGGTTTGT 120  
CCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGAGCGTGA  
121 CGTTCCTGTGGGAGTACTAGAGGGCTCGGGACTCCAGTGTACGCACACACCTGCACT 180  
GCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTGCATAATG  
181 CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGACCTCCACGTATTAC 240  
CCAAGACAAAGCCCGGGAGGAGCAGTACAAGCAGCAGTACCGTGTGGTACGCTCCTCA  
241 GGTTCCTGTTTCGGCGCCCTCTCTGTCATGTTGTGTCATGGCACACCGTCCGAGGAGT 300  
CCGTCTCTGACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTTCTTCAACAAG  
301 GGCAGGACGTGGTCTGACCGACTTACCGTTCTCTCATGTTACGTTCCAGAGGTTGTTTC 360  
CCCTCCCGACCCCATCGAGAAAACATCTCCAAAGCCAAAGGGCAGCCCGAGAACAC  
361 GGGAGGCTCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG 420  
AGGTGTACACCCCTGCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGACGCTGACCT  
421 TCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGTTCTTGGTCAAGTCGAGCTGGA 480  
GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCGAGC  
481 CGGACCAAGTTTCCGAAGATAGGGTCGCTGTAGCGGACCTCACCTCTCGTTACCGCTCG 540  
CGGAAACAACTACAAGACACCGCTCCGCTGCTGGACTCCGACGGCTCCTTCTCTCTCT  
541 GCCTCTGTGTGATGTTCTGGTGGAGGGGACGACCTGAGGGCTGCCGAGGAAGAGGAGA 600  
ACAGCAAGCTCACCGTGGACAAAGCAGGTGGCAGCAGGGGAAAGCTCTTCTATGCTCCG  
601 TGTGTTTCGAGTGCGACCTGTTCTCGTCCACCGTGGTCCCTTTCGAGAAGAGTACGAGGC 660  
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCTCTCCTGTCTCCGGGTA  
661 ACTACGTACTCCGAGACGTGTTGGTGATGTGCTTCTCTCGGAGAGGACAGAGGCCATC 720  
AAGGTGGAGGTGGTGGTGGAGGTACTTACTCTTGCACCTTCGGCCCGCTGACTTGGGTTT  
721 TTCCACCTCCACCAACCTCATGAATGAGAACGGTGAAGCCGGGCGACTGAACCCAAA 780  
BamHI  
|  
GCAAAACCGCAGGGTGGTTAATCTCGTGGATCC  
781 CGTTTGGCGTCCCAACCAATTAGAGCACCTAGG 812  
K P Q G G \*

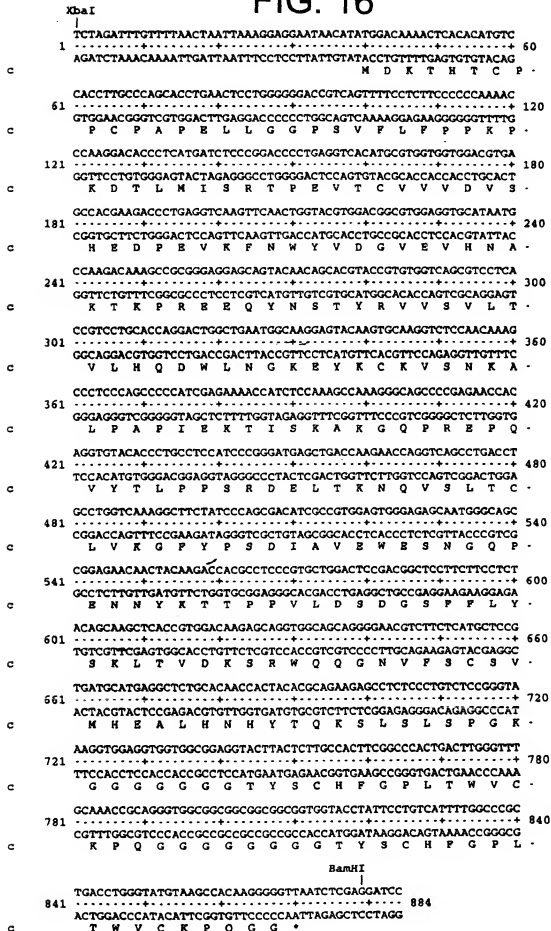
# FIG. 14



# FIG. 15

XbaI  
|  
1 TCTAGATTTGAGTTTAACTTTTAGAAGGAGGAATAAAATATGGGAGGTACTTACTCTTG 60  
AGATCTAAACTCAAATTTGAAATCTTCCTCTCTTATTTTATACCTTCATGAATGAGAAC  
M G G T Y S C  
b  
61 CCACCTTCGGCCCACTGACTTGGGTTGCAACCGCAGGGTGCGCGCGCGCGCGGTGG 120  
GGTGAAGCCGGGTGACTGAACCCAAACGTTTGGCGTCCACCGCGCGCGCGCGCGCACC  
H F G P L T W V C K P Q G G G G G G G G  
b  
121 TACCTATTCTGTCTATTTTGGCCCGCTGACCTGGGTATGTAAGCCACAAGGGGTGGGG 180  
ATGGATAAGGACAGTAAACCGGGGACTGGACCCATACATTCGGTGTTCGCCACCCCT  
T Y S C H F G P L T W V C K P Q G G G G G  
b  
181 AGGCGGGGGGACAAAACCTCACACATGTCCACCTTGCCACGACCTGAACCTCTGGGGGG 240  
TCCGCCCCCTCTTTTGAAGTGTGTACAGGTGGAACGGGTCTGGACTTGAGGACCCCG  
G G G D K T H T C P P C P A F E L L G G  
b  
241 ACCGTCAAGTTTCTCTTCCCGCCAAAGGACACCTCATGATCTCCCGACCCG 300  
TGGCAGTCAAAAGGAGAGGGGGTTTGGGTTCTGTGGAGTACTAGAGGGCTCGGG  
P S V F L F P P K P K D T L M I S R T P  
b  
301 TGAGGTCACATCGCTGGTGGACGTGAGCCAGGACCCCTGAGGTCAAGTTCAACTG 360  
ACTCCAGTGTACGACCAACACCTGCCTCGTCTCTGGGACTCCAGTTCAGTTGAC  
E V T C V V V D V S H E D P E V K F N W  
b  
361 GTACGTGGACGGCGTGGAGGTGCATATGCCAAGACAAGCCGCGGGAGGAGTACAA 420  
CATGCACTCGCCGACCTCCACGTATTACGGTTCTGTTTCCGCGCCCTCTCTCATGTT  
Y V D G V E V H N A K T K P R E E Q Y N  
b  
421 CAGACGTACCGTGTGGTCAAGCTCTCACCGTCTGACACGAGTCTGGTGAATGGCAA 480  
GTCTGCATGGCACACCACTGCGAGGAGTGGCAGGACGTGGTCTGACCGACTTACGGT  
S T Y R V V S V L T V L H Q D W L N G K  
b  
481 GGAGTACAAGTGCAAGGTCTCCACAAGCCCTCCAGCCCCCATCGAGAAAACCATCTC 540  
CCTCATGTTCAAGTCCAGAGGTGTTTCCGGAGGGTCCGGGGTAGCTCTTTTGGTAGAG  
E Y K C K V S N K A L P A P I E K T I S  
b  
541 CAAAGCCAAAGGCGAGCCCCGAGAACCACAGGTGTACACCTCGCCCCATCCCGGATGA 600  
GTTTCGGTTTCCCGTCCGGGCTCTTGGTCTCACATGTGGGACGGGGTAGGGCCCTACT  
K A K G Q P R E F Q V Y T L P P S R D E  
b  
601 GCTGACCAAGAACCAGGTGACCTGACCTGGTGGTCAAGGGCTCTATCCAGCGACAT 660  
CGACTGGTCTTGGTCCAGTGGACTGGACGGACAGTTTCCGAAGATAGGGTCTGTTA  
L T K N Q V S L T C L V K G F Y P S D I  
b  
661 CGCCGTGGAGTGGGAGCAATGGGACGCGGAGAACACTACAAGACACGCTCCCGT 720  
CGGCACTCAACCTCTCTGTTACCCGTCCGCTCTCTGTTGATGTTCTGGTGGAGGGCA  
A V E W E S N G Q P E N N Y K T T P P V  
b  
721 GCTGGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCCTGGACAAGAGCAGGTG 780  
CGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCAGCTGTCTCTGTCAC  
L D S D G S F F L Y S K L T V D K S R W  
b  
781 GCACGAGGGGAAGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCACTACAC 840  
CGTCTGCTCCCTTGCAGAAAGTACGAGGACTACGTAAGTCCGAGACGTGTGTTGATGTG  
Q G C N V F S C S V M H E A L H N H Y T  
b  
BanHI  
|  
841 GCAGAAGAGCCTCTCCCTGTCTCCGGTAAATATGGATCC 881  
CGTCTTCTCGGAGGGGACAGGCCCATTTATTACCTAGG  
Q K S L S L S P G K \*

# FIG. 16





## FIG. 17A

[*Aat*II sticky end] 5' GCGTAACGTATGCATGGTCTCC-  
(position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG-

-CCATGCGAGAGTAGGGAAGTCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-  
-GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGTCTTCGAGATCAGCTTTCTGA-

-GGGCCTTTCGTTTTATCTGTTGTTTGTGCGTGAAACGCTCTCTGAGTAGGACAAATCCCG-  
-CCCGGAAAGCAAAATAGACAACAACAGCCACTTCGAGAGGACTCATCTGTTTATAGCGG-

-CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCGGAGGGTGCGGGCAGGACGCCCGC-  
-GCCCTCGCTAAACTTGCAACGCTTCGTTGCCGGGCCCTCCACCGCCCGTCTCGGGCG-

-CATAAATGCCAGGCATCAAATTAAGCAGAAGGCCATCTGACGGATGGCCTTTTTGCGT-  
-GTATTTGACGGTCCGTAGTTTAATTCGTCTCCGGTAGGACTGCCTACCGGAAAAACGCA-

*Aat*II

-TTCTACAAACTCTTTTGTATTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAA-  
-AAGATGTTTGAGAAAAAAATAAAAGATTTATGTAAAGTTTATACCTCGAGCATGAATTG-

-TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAAAATTGCTTTAGAAATACTTTGGCAGC-  
-AAAATTTTCATACCCGTTAGTTTAAAGAGGACAAATTTAACGAAATCTTTATGAAACCGCTC-

-GGTTTGTGTATTGAGTTTCATTTGCGCATTGTTTAAATGGAAAGTGACCGTGCCTTAC-  
-CCAAACAAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCAGTGGCACGCGAATG-

-TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCTTCGCATGCCACGCTAAAC-  
-ATGTCGGATTATAAAACCTTTATAGGTTCTCGAAAAAGGAAGCGTACGGTGCGATTG-

-ATTCTTTTTCTCTTTGGTTAAATCGTTGTTGATTTATTATTTGCTATATTTATTTTTTC-  
-TAAGAAAAAGAGAAAAACCAATTTAGCAACAACTAAATAATAACGATATAATAAAAAAG-

-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTATACACGCATGTAATAA-  
-CTATTAATAGTTGATCTCTCTCTGTTAATTACCATACAAGTATGTGCGTACATTTTTAT-

-AATCTATCTATATAGTTGTCTTTCTCTGAATGTGCAAACTAAGCATTCGGAAGCCATTAT-  
-TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTCGAAGGCTTACGACCAAT-

-TAGCAGTATGAATAGGGAACATAACCCAGTGATAAGACCTGATGATTTTCGCTCTTTAA-  
-ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAAT-

-TTACATTTGGAGATTTTTATTTACAGCATTTGTTTCAAATATATCCAATTAATCGGTT-  
-AATGTAAACCTCTAAAAAATAAATGTCTGAACAAAAGTTTATATAAGGTAAATTAGGCCAC-

-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAATTAGCGTCATCAT-  
-TTACTAACTCAATCTTATTAGATGATATCCTAGTATAAAAAATTTAATCGAGTAGTA-

-AATATTGCCCTCATTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-  
-TTATAACGGAGGTAAAAAATCCCATTAATAGGCTTTAACTTTATAGTCTAAATTTAGGATC-

-AATGAGGATAAATGATCGCGAGTAAATAATATTCACAAATGACCAATTTAGTCATATCAG-  
-TTACTCTTATTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAATCAGTATAGTC-

-ATAAGCATTGATTAATATCATTTATTGCTTCTACAGGCCTTAATTTTATTAATTTATCTGT-  
-TATTCTGAACATAATATAGTAATAACGAAGATGTCCGAAATAAAAATAATTAATAAGACA-

-AAGTGCCTGTCGGCATTTATGCTTTTCATACCCATCTCTTTATCTCTTACCTATTGTTTGT-  
-TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGAATAACAAACAG-

-GCAAGTTTTGCGTGTTATATATCATTAAAAACGGTAATAGATTGACATTTGATTCTAATAA-  
-CGTTCAAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT-

## FIG. 17B

- ATTGGATTTTGTCACTATTATATCGCTTGAAATACAATTGTTTAACATAAGTACCTG -  
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC -  
  
- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAAATCGATTTGATT -  
- ATCCTAGCATGTCCAAATGCGTTCCTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -  
  
- CTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -  
- GATCTAAACAAAATTGATTAATTTCCCTCCTTATGTATACCAATTGCGCAACCTTAAGCT -  
  
- GCTCACTAGTGTGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -  
- CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT -  
  
- GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -  
- CTCCTTCTTCTTCTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT -  
  
- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGG -  
- TGATCGTATTGGGGAACCCCGGAGATTTGCCCAAGAACTCCCCAAAAAACGACTTTCCTCC -  
  
- AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end]  
- TTGGCGAGAAGTGCAGAAAGTG 5' (position #5904 in pAMG21)

FIG.18A - 1

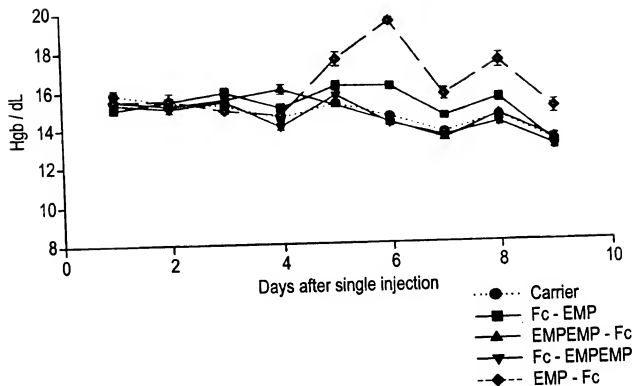


FIG.18A - 2

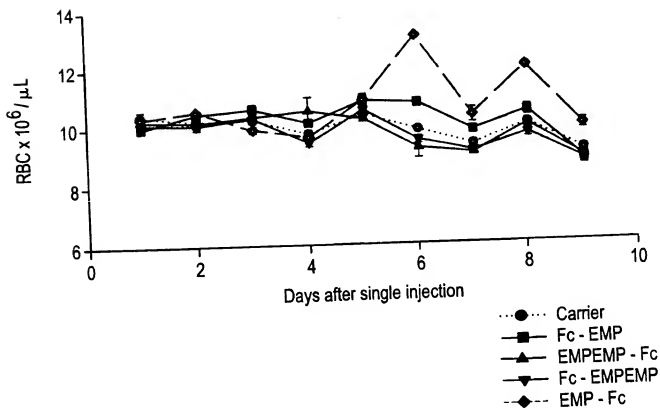


FIG.18A - 3

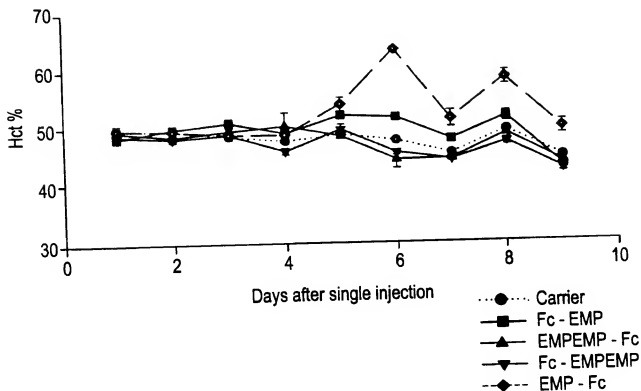


FIG.18B - 1

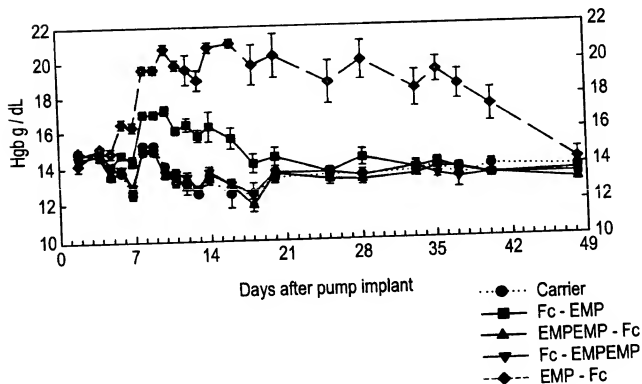


FIG.18B - 2

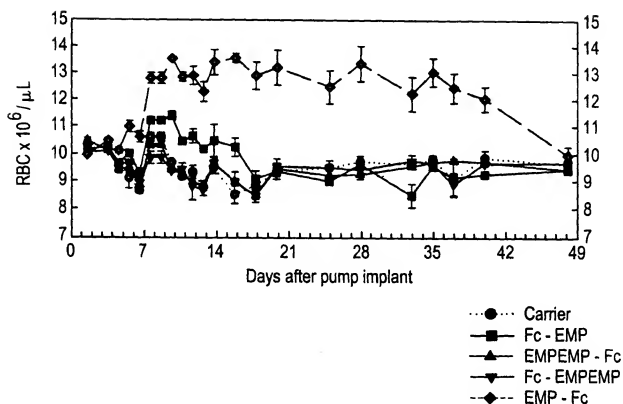
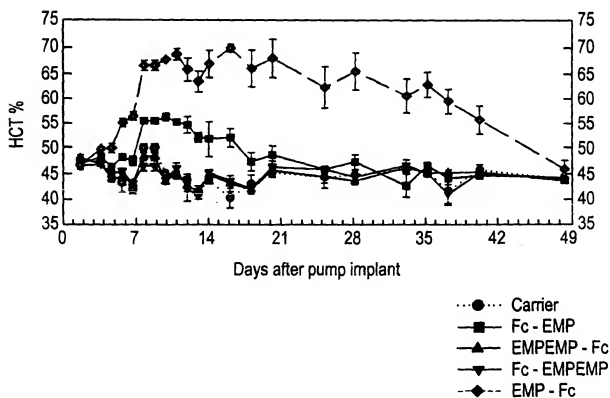


FIG.18B - 3



# FIG. 19A

NdeI  
1  
CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGACCG  
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTGAGGCCCTGAGGACCCCTCGGC 60

a M D K T H T C P P C P A P E L L G G P  
TCAGTCTTCCTCTTCCCCCAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAG  
61 AGTCAGAAGGAGAAGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCTTGGGACTC 120

a S V F L F P P K P K D T L M I S R T P E  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAC  
121 CAGTGTACGCACACACCTGCACCTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180

a V T C V V V D V S H E D P E V K F N W Y  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
181 CACCTCGCCGACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCAATGTGTGCG 240

a V D G V E V H N A K T K P R E E Q Y N S  
ACGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACCAAGACTGGCTGAATGGCAAGGAG  
241 TGCATGGCACACAGTCGACAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCTC 300

a T Y R V V S V L T V L H Q D W L N G K E  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAA  
301 ATGTTACGTTCCAGAGGTTGTTTCGGGAGGTCGGGGTAGCTCTTTTGGTAGAGGTTT 360

a Y K C K V S N K A L P A P I E K T I S K  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTTGCCCCCATCCCGGGATGAGCTG  
361 CGGTTTCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGAC 420

a A K G Q P R E P Q V Y T L P P S R D E L  
ACCAAGAACCAAGGTCAAGCTGACCTGCCTGGTCAAAGGCTTCTATCCACGCGACATCGCC  
421 TGGTCTTGGTCCAGTCGGACTGGACGGACCAAGTTCCGAAGATAGGGTCGCTGTAGCGG 480

a T K N Q V S L T C L V K G F Y P S D I A  
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCCGTGTG  
481 CACCTCACCTCTCGTTACCCGTCGGCTCTTGTGTGATGTTCTGGTGGGAGGGCAGGAC 540

a V E W E S N G Q P E N N Y K T T P P V L  
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
541 CTGAGGCTCGCCAGGAAGAAGGAGATGTCGTTTCGAGTGGACCTGTTCTCGTCCACCGTC 600

a D S D G S P F L Y S K L T V D K S R W Q

## FIG. 19B

```

601  CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
    .....+.....+.....+.....+.....+.....+.....+.....+.....+ 660
    GTCCCCTTGCAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a    Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  .

    AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC
661  .....+.....+.....+.....+.....+.....+.....+.....+.....+ 720
    TTCTCGGAGAGGGACAGAGGCCATTTCACCTCCACCACCCTGAAGGACGGCGTGATG

a    K  S  L  S  L  S  P  G  K  G  G  G  G  G  D  F  L  P  H  Y  .

                                BamHI
                                |
    AAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC
721  .....+.....+.....+.....+.....+.....+.....+.....+.....+ 757
    TTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG

a    K  N  T  S  L  G  H  R  P  .
    
```

NdeI  
|  
CATATGGACTTCCTGCGCACTACAAAAACACCTCTCTGGGTACCGTCCGGGTGGAGGC  
1 +-----+ 60  
GTATACCTGAAGGACGCGTGATGTTTTTGTGGAGAGACCCAGTGGCAGGCCACCTCCG  
a M D F L P H Y K N T S L G H R P G G G -  
GGTGGGGACAAACTCACACATGTCACCTTGCCACGACCTGAACCTCTGGGGGACCG  
61 +-----+ 120  
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCTGGACTTGAGGACCCCCCTGGC  
a G G D K T H T C P P C P A P E L L G G P -  
TCAGTTTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAG  
121 +-----+ 180  
AGTCAAAAGGAGAAGGGGGTTTTGGTTCTCTGTGGAGTACTAGAGGGCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTCAACTGGTAC  
181 +-----+ 240  
CAGTGTACGACACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
GTGGACGGCGTGAGGAGTGCAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
241 +-----+ 300  
CACCTCGCGACCTCCACGTATTACGGTTCTGTTTCGGCGCCTCTCTCGTCATGTTGTCG  
a V D G V E V H N A K T K P R E E Q Y N S -  
ACGTACCGTGTGGTCAGCGTCTCTACCGTCTGCAACGAGACTGGTGAATGGCAAGGAG  
301 +-----+ 360  
TGCATGGCACACAGTCGCAGGAGTGGCAGGACGTGCTCTGACCGACTTACCGTCTCCT  
a T Y R V V S V L T V L H Q D W L N G K E -  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAA  
361 +-----+ 420  
ATGTTCCAGTTCACAGAGTTGTTTCGGGAGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K K C K V C K C C G A G A A C A G L T P A P I E K T I S K -  
GCCAAGGGCAGCCCCGAGAAACACAGGTGTACACCTTGCCCCATGCCGGGATGAGCTG  
421 +-----+ 480  
CGGTTTCCCGTCGGGGCTCTTGTGTGCACATGTGGGACGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
ACCAAGAACAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC  
481 +-----+ 540  
TGGTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCTCCCGTGTG  
541 +-----+ 600  
CACCTCACCTCTCGTTACCCGTCGCGCTCTGTTGATGTTCTGGTGGGAGGGCAGCAGC  
a V E W E S N G O P E N N Y K T T P P V L -



# FIG. 20B

```

601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 660
    .....+.....+.....+.....+.....+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a   D S D G S F F L Y S K L T V D K S R W Q -

    CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAGCGAG
661 .....+.....+.....+.....+.....+ 720
GTCCCCTTGCAGAAGAGTACGAGGCACCTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q G N V P S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
    AAGAGCCTCTCCCTGTCTCCGGGTAATAATGGATCCGCGG
721 .....+.....+.....+.....+ 761
    TTCTCGGAGAGGGACAGAGGCCATTATTACCTAGGCGCC

a   K S L S L S P G K *
```

# FIG. 21A

NdeI  
CATATGGCAAAAACTCACACATGCCACCTTGTCAGCTCCGGAACCTCTGGGGGGACCG  
1 .....+ 60  
GTATACCTGTTTGTAGTGTGTACAGGTGGAACAGGTGAGGCCCTTGAGGACCCCTTGGC  
a M D K T H T C P P C P A P E L L G G P .  
TCAGTCTTCTCTTCCCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCTGAG  
61 .....+ 120  
AGTCAGAAGGAAAGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGCCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E .  
GTCACATGCGTGGTGGTGGAGCTGAGCCAGAACCCCTGAGGTCAAGTTCAACTGGTAC  
121 .....+ 180  
CAGTTGACGACCAACACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y .  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
181 .....+ 240  
CACCTGCCGACCTCCAGCTATTACGGTTCTGTTCGGCGCCCTCCTCGTCAATGTTGTCG  
a V D G V E V H N A K T K P R E E Q Y N S .  
ACGTCACCGTGTGGTCAAGCTCCTCACCGTCTGCACAGGACTGGTGAATGGCAAGGAG  
241 .....+ 300  
TGCAATGGCACACAGTGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCTCTC  
a T Y R V V S V L T V L H Q D W L N G K E .  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAA  
301 .....+ 360  
ATGTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K .  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTG  
361 .....+ 420  
CGGTTTCCCGTCGGGGCTCTTGTGTGTCACATGTGGACGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L .  
ACCAAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC  
421 .....+ 480  
TGGTTCTTGGTCTCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A .  
GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACACCGCTCCCGTGTG  
481 .....+ 540  
CACCTCACCTCTCGTTACCCGTCGGCTCTTGTGTATGTTCTGGTGGGAGGGCAGCAG  
a V E W E S N G Q P E N N Y K T T P P V L .  
GACTCCGACGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
541 .....+ 600  
CTGAGGCTCGCCAGGAAGAAGGAGATGTCGTTGAGTGGACACCTGTTCTCTGTCACCGTC  
a D S D G S F F L Y S K L T V D K S R W Q .

## FIG. 21B

```

601  CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG  660
      -----+-----+-----+-----+-----+-----+-----+
      GTCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a    Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -
      AAGAGCCTCTCCCTGTCTCCGGGTAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGT
661  TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAGCTTACCTGGGGCCCA  720
      -----+-----+-----+-----+-----+-----+-----+
a    K  S  L  S  L  S  P  G  K  G  G  G  G  G  F  E  W  T  P  G  -
                                     BamHI
                                     |
      TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
721  ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC  763
      -----+-----+-----+-----+-----+-----+-----+
a    Y  W  Q  P  Y  A  L  P  L  *
```

# FIG. 22A

NdeI  
|  
1 CATATGTTTCAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC 60  
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG

a M F E W T P G Y W Q P Y A L P L G G G -

61 GGTGGGGACAAAACTCACACATGTCCACCTTGCCACGACCTGAACCTCTGGGGGGACCG 120  
CCACCCCTGTTTTAGTGTGTACAGGTGGAACGGTCTGTGGACTTGAGGACCCCCCTGGC

a G G D K T H T C P P C P A P E L L G G P -

121 TCAGTTTTCTCTTCCCCC AAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAG 180  
AGTCAAAAGGAGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

181 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAGATTCAACTGGTAC 240  
CAGTGTACGCCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

241 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAGC 300  
CACCTGCCGCACCTCCACGTATTACGGTCTGTTCGGGGCCCTCCTCGTCATGTTGTGCG

a V D G V E V H N A K T K P R E E Q Y N S -

301 ACGTACCGTGTGGTCCAGCGTCTCACCCTCCTGCACCCAGGACTGGCTGAATGGCAAGSAG 360  
TGATGGCACCAGTCCGAGGAGTGGCAGGACGTGGTCTTGACCGACTTACCGTTCGCTC

a T Y R V V S V L T V L H Q D W L N G K E -

361 TACAAGTGCAAGGTTCTCAACAAAGCCCTCCAGCCCCCATCGAGAAAAACCATCTCCAAA 420  
ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCCGGGGGTAGCTCTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

421 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTTGCCCCCATCCCGGATGAGCTG 480  
CGGTTTCCCGTCCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

481 ACCAAGAACCAGGTGACGCTGACCTGGTCAAAGGCTTCTATCCACGACGACATCGCC 540  
TGGTTCTTGGTCCAGTCCGACTGGACGGACAGTTTCCGAAGATAGGGTCGTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

541 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACATAAGACACGCCTCCCGTGTG 600  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTCCGGAGGGACACGAC

a V E W E S N G Q P E N N Y K T T P P V L -



# FIG. 23A

NdeI  
 |  
 CATATGGACAAAACCTCACACATGTCCACCGTGCCACGACCTGAACTCTGGGGGGACCG 60  
 1 -----+-----+-----+-----+-----+-----+-----+-----+  
 GTATACCTGTTTGTGAGTGTGTACAGGTGGCAGGGTCTGTGGAAGTGGAGGACCCCTGGC  
 a M D K T H T C P P C P A P E L L G G P -  
 TCAGTTTTCTCTTCCCCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAG 61  
 -----+-----+-----+-----+-----+-----+-----+-----+ 120  
 AGTCAAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
 a S V F L F P P K P K D T L M I S R T P E -  
 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAAGTTGATC 121  
 -----+-----+-----+-----+-----+-----+-----+-----+ 180  
 CAGTGTACGACCAACCACTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
 a V T C V V V D V S H E D P E V K F N W Y -  
 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 181  
 -----+-----+-----+-----+-----+-----+-----+-----+ 240  
 CACCTGCCGACACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCTCGTCAATGTTGTG  
 a V D G V E V H N A K T K P R E E Q Y N S -  
 ACGTACCGTGTGGTCAAGCTCCTCACCCTGCTGACCCAGGACTGGCTGAATGGCAAGGAG 241  
 -----+-----+-----+-----+-----+-----+-----+-----+ 300  
 TGCATGGCACCAAGCTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTC  
 a T Y R V V S V L T V L H Q D W L N G K E -  
 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAA 301  
 -----+-----+-----+-----+-----+-----+-----+-----+ 360  
 ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTTCGGGGGTAGCTCTTTTGGTAGAGGTTT  
 a Y K C K V S N K A L P A P I E K T I S K -  
 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTG 361  
 -----+-----+-----+-----+-----+-----+-----+-----+ 420  
 CGGTTTCCCGCTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGAC  
 a A K G Q P R E P Q V Y T L P P S R D E L -  
 ACCAAGAACCAGGTCAAGCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC 421  
 -----+-----+-----+-----+-----+-----+-----+-----+ 480  
 TGGTTCCTGGCTCAGTCCGACTGGACGGACCAAGTTCCGAAGATAGGGTCTGTAGCGG  
 a T K N Q V S L T C L V K G F Y P S D I A -  
 GTGGAGTGGGAGGACAAATGGGCAGCCGGAGAACAACATAAGACCACGCCTCCCGTGTG 481  
 -----+-----+-----+-----+-----+-----+-----+-----+ 540  
 CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGACGAC  
 a V E W E S N G Q P E N N Y K T T P P V L -  
 GACTCCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 541  
 -----+-----+-----+-----+-----+-----+-----+-----+ 600  
 CTGAGGCTCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC  
 a D S D G S F P F L Y S K L T V D K S R W Q -

## FIG. 23B

```

601  CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
      .....+.....+.....+.....+.....+.....+.....+.....+.....+
      GTCCCCCTTGCAGAAAGAGTACGAGGCACCTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

      AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGGTGAACCGAACTGTGAC
661  .....+.....+.....+.....+.....+.....+.....+.....+.....+ 720
      TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACCTTGGCTTGACACTG

a      K  S  L  S  L  S  L  S  P  G  K  G  G  G  G  G  V  E  P  N  C  D  -

                                     BamHI
                                     |
      ATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTGTAACCTCGAGGATCC
721  .....+.....+.....+.....+.....+.....+.....+.....+.....+ 773
      TAGGTACAATACACCCCTTACCCTTACAAAACCTGCAGACATTGAGCTCCTTAGG

a      I  H  V  M  W  E  W  E  C  F  E  R  L  *
```

[illegible]



## FIG. 24B

```

601 CCTCCCGTGTGGACTCCGACGGCTCCTTCTCCTCTACAGCAAGCTCACC GTGGACAAG
    .....+.....+.....+.....+.....+ 660
    GGAGGGCAGCACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTC
a   P P V L D S D G S F F L Y S K L T V D K -
    AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAAC
661 .....+.....+.....+.....+.....+ 720
    TCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG
a   S R W Q Q G N V F S C S V M H E A L H N -
                                     BamHI
                                     |
    CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATAACTCGAGGATCC
721 .....+.....+.....+.....+.....+ 773
    GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG
a   H Y T Q K S L S L S P G K *
    
```

# FIG. 25A

NdeI  
|  
CATATGGCAAAAACACACATGTCCACCTTGTCAGCTCCGGAACCTCTGGGGGACCG  
1 .....+..... 60  
GTATACCTGTTTGTAGTGTGTACAGGTGGAACAGGTCGAGGCCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

TCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAG  
61 .....+..... 120  
AGTCAGAAAGAGAAGGGGGGTTTGGGTTCTGTGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC  
121 .....+..... 180  
CAGTGTACGCACCAACCTGCACCTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
181 .....+..... 240  
CACCTGCCGCACCTCCAGTATTACGGTTCTGTTTCGGGCGCCTCCTCGTCATGTTGTCTG

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAAGCTCCTCACCGTCTCTGACAGGACTGGCTGAATGGCAAGGAG  
241 .....+..... 300  
TGATGTGCACACCAAGTGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTCTCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA  
301 .....+..... 360  
ATGTTACAGTTCACAGGTTGTTTCGGGAGGGTCGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGGACGCCCGGAGAACCACAGGTGTACACCTTGCCCCATCCCGGATGAGCTG  
361 .....+..... 420  
CGGTTTCCCGTGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACAGGTCAAGCTGACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCC  
421 .....+..... 480  
TGGTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGAGCCGGAGAACAACACAGGACAGGCTCCCGTGGCTG  
481 .....+..... 540  
CACCTCACCTCTCGTTACCCGTCGGCTCTTGTGTGATGTTCTGGTGGGAGGGGACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

GACTCCGAGCGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
541 .....+..... 600  
CTGAGGCTGCCAGGAAGAAGGAGATGTCGTTTCGAGTGGACCTGTCTCTGCTCCACCGTC

a D S D G S P F L Y S K L T V D K S R W Q -

## FIG. 25B

```

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
    .....+.....+.....+.....+.....+
    GTCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a    Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  *

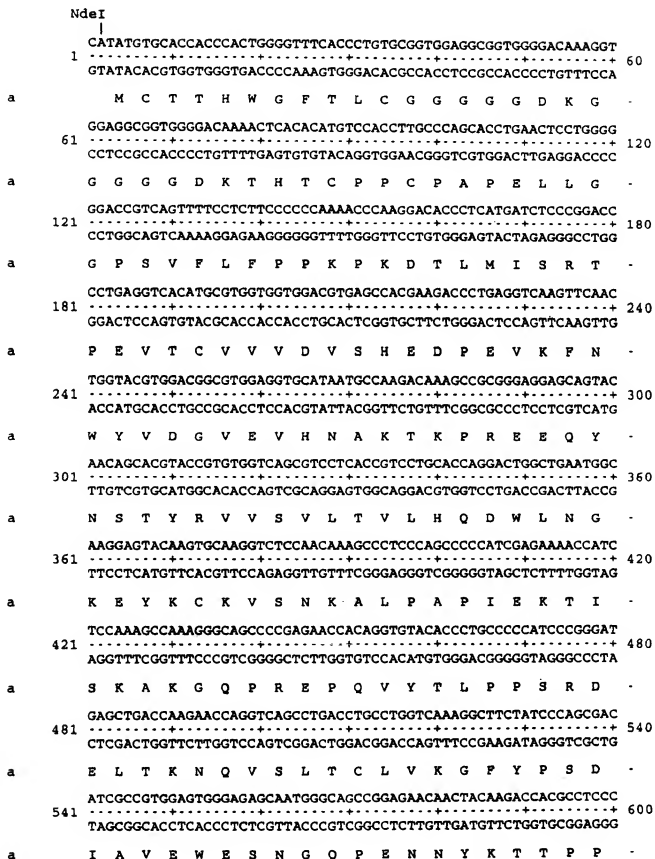
    AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCACTGGGGT
661 .....+.....+.....+.....+.....+ 720
    TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA

A    K  S  L  S  L  S  P  G  K  G  G  G  G  G  C  T  T  H  W  G  *

          BamHI
          |
    TTCACCCTGTGCTAATGGATCCCTCGAG
721 .....+.....+.....+.....+ 748
    AAGTGGGACACGATTACCTAGGGAGCTC

a    F  T  L  C  *
  
```

FIG. 26A



## FIG. 26B

```

      GTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG
601  -----+-----+-----+-----+-----+-----+-----+-----+ 560
      CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCC
a      V L D S D G S F F L Y S K L T V D K S R .

      TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
661  -----+-----+-----+-----+-----+-----+-----+ 720
      ACCGTCGTCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a      W Q Q G N V F S C S V M H E A L H N H Y .

                                     BamHI
                                     |
      ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721  -----+-----+-----+-----+-----+-----+ 763
      TCGCTCTTCTCGGAGAGGGACAGAGGCCATTTATTACCTAGG
a      T Q K S L S L S P G K *
```